



CGGGGAACA AGATGTGAAC TGTTTTCCCT CCCAGAAGA AGAGGCCCTT TTTTCCCTC	60
CCGCGAAGGC CAATGTTCTG AAAAAAGCTC TAG <sup>*</sup> ATG GGA ATG GCC TGC CTT ACA	114
Met Gly Met Ala Cys Leu Thr	
1 5	
<sup>*</sup> ATG ACA GAA <sup>*</sup> ATG GAG GCA ACC TCC ACA TCT CCT GTA CAT CAG AAT GGT	162
Met Thr Glu Met Glu Ala Thr Ser Thr Ser Pro Val His Gln Asn Gly	
10 15 20	
GAT ATT CCT GGA AGT GCT AAT TCT GTG AAG CAG ATA GAG CCA GTC CTT	210
Asp Ile Pro Gly Ser Ala Asn Ser Val Lys Gln Ile Glu Pro Val Leu	
25 30 35	
CAA GTG TAT CTG TAC CAT TCT CTT GGG CAA GCT GAA GGA GAG TAT CTG	258
Gln Val Tyr Leu Tyr His Ser Leu Gly Gln Ala Glu Gly Glu Tyr Leu	
40 45 50 55	
AAG TTT CCA AGT GGA GAG TAT GTT GCA GAA GAA ATT TGT GTG GCT GCT	306
Lys Phe Pro Ser Gly Glu Tyr Val Ala Glu Glu Ile Cys Val Ala Ala	
60 65 70	
TCT AAA GCT TGT GGT ATT ACG CCT GTG TAT CAT AAT ATG TTT GCG TTA	354
Ser Lys Ala Cys Gly Ile Thr Pro Val Tyr His Asn Met Phe Ala Leu	
75 80 85	
ATG AGT GAA ACC GAA AGG ATC TGG TAC CCA CCC AAT CAT GTC TTC CAC	402
Met Ser Glu Thr Glu Arg Ile Trp Tyr Pro Pro Asn His Val Phe His	
90 95 100	
ATA GAC GAG TCA ACC AGG CAT GAC ATA CTC TAC AGG ATA AGG TTC TAC	450
Ile Asp Glu Ser Thr Arg His Asp Ile Leu Tyr Arg Ile Arg Phe Tyr	
105 110 115	
TTC CCT CAT TGG TAC TGT AGT GGC AGC AGC AGA ACC TAC AGA TAC GGA	498
Phe Pro His Trp Tyr Cys Ser Gly Ser Ser Arg Thr Tyr Arg Tyr Gly	
120 125 130 135	
GTG TCC CGT GGG GCT GAA GCT CCT CTG CTT GAT GAC TTT GTC ATG TCT	546
Val Ser Arg Gly Ala Glu Ala Pro Leu Leu Asp Asp Phe Val Met Ser	
140 145 150	

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FIG.1A

CC C	
TAC CTT TTT GCT CAG TGG CCG CAT GAT TTT GTT CAC GGA TGG ATA AAA	594
Tyr Leu Phe Ala Gln Trp Arg His Asp Phe Val His Gly Trp Ile Lys	
S P 160 165	
155	
GTA CCT GTG ACT CAT GAA ACT CAG GAA GAG TGT CTT GGG ATG GCG GTG	642
Val Pro Val Thr His Glu Thr Gln Glu Glu Cys Leu Gly Met Ala Val	
170 175 180	
TTA GAC ATG ATG AGA ATA GCT AAG GAG AAA GAC CAG ACT CCA CTG GCT	690
Leu Asp Met Met Arg Ile Ala Lys Glu Lys Asp Gln Thr Pro Leu Ala	
185 190 195	
GTC TAT AAC TCT GTC AGC TAC AAG ACA TTC TTA CCA AAG TGC GTT CGA	738
Val Tyr Asn Ser Val Ser Tyr Lys Thr Phe Leu Pro Lys Cys Val Arg	
200 205 210 215	
GCG AAG ATC CAA GAC TAT CAC ATT TTA ACC CCG AAG CGA ATC AGG TAC	786
Ala Lys Ile Gln Asp Tyr His Ile Leu Thr Arg Lys Arg Ile Arg Tyr	
220 225 230	
AGA TTT CGC AGA TTC ATT CAG CAA TTC AGT CAA TGT AAA GCC ACT GCC	834
Arg Phe Arg Arg Phe Ile Gln Gln Phe Ser Gln Cys Lys Ala Thr Ala	
235 240 245	
AGG AAC CTA AAA CTT AAG TAT CTT ATA AAC CTG GAA ACC CTG CAG TCT	882
Arg Asn Leu Lys Leu Lys Tyr Leu Ile Asn Leu Glu Thr Leu Gln Ser	
250 255 260	
GCC TTC TAC ACA GAA CAG TTT GAA GTA AAA GAA TCT GCA AGA GGT CCT	930
Ala Phe Tyr Thr Glu Gln Phe Glu Val Lys Glu Ser Ala Arg Gly Pro	
265 270 275	
TCA GGT GAG GAG ATT TTT GCA ACC ATT ATA ATA ACT GGA AAC GGT GGA	978
Ser Gly Glu Glu Ile Phe Ala Thr Ile Ile Ile Thr Gly Asn Gly Gly	
280 285 290 295	
ATT CAG TGG TCA AGA GGG AAA CAT AAG GAA AGT GAG ACA CTG ACA GAA	1026
Ile Gln Trp Ser Arg Gly Lys His Lys Glu Ser Glu Thr Leu Thr Glu	
300 305 310	

FIG.1B

CAG GAC GTA CAG TTA TAT TGT GAT TTC CCT GAT ATT ATT GAT GTC AGT	1074
Gln Asp Val Gln Leu Tyr Cys Asp Phe Pro Asp Ile Ile Asp Val Ser	
315 320 325	
l c g g c	
ATT AAG CAA GCA AAC CAG GAA TGC TCA AAT GAA AGT AGA ATT GTA ACT	1122
Ile Lys Gln Ala Asn Gln Glu Cys Ser Asn Glu Ser Arg Ile Val Thr	
330 335 T 340 V	
c g g c g g c	
GTC CAT AAA CAA GAT GGT AAA GTT TTG GAG ATA GAA CTT AGC TCA TTA	1170
Val His Lys Gln Asp Gly Lys Val Leu Glu Ile Glu Leu Ser Ser Leu	
345 350 355	
l g	
AAA GAA GCC TTG TCA TTC GTG TCA TTA ATT GAC GGG TAT TAC AGA CTA	1218
Lys Glu Ala Leu Ser Phe Val Ser Leu Ile Asp Gly Tyr Tyr Arg Leu	
360 365 370 375	
g t t c	
ACT GCG GAT GCG CAC CAT TAC CTC TGC AAA GAG GTG GCT CCC CCA GCT	1266
Thr Ala Asp Ala His His Tyr Leu Cys Lys Glu Val Ala Pro Pro Ala	
380 385 390	
t q t t	
GTG CTC GAG AAC ATA CAC AGC AAC TGC CAC GGC CCA ATA TCA ATG GAT	1314
Val Leu Glu Asn Ile His Ser Asn Cys His Gly Pro Ile Ser Met Asp	
395 400 405	
c o o g	
TTT GCC ATT AGC AAA CTA AAG AAG GCG GGT AAC CAG ACT GGA CTA TAT	1362
Phe Ala Ile Ser Lys Leu Lys Lys Ala Gly Asn Gln Thr Gly Leu Tyr	
410 415 420	
q t t c	
GTG CTA CGA TGC AGC CCT AAG GAC TTC AAC AAA TAC TTT CTG ACC TTT	1410
Val Leu Arg Cys Ser Pro Lys Asp Phe Asn Lys Tyr Phe Leu Thr Phe	
425 430 435	
c t q	
GCT GTT GAG CGA GAA AAT GTC ATT GAA TAT AAA CAC TGT TTG ATT ACG	1458
Ala Val Glu Arg Glu Asn Val Ile Glu Tyr Lys His Cys Leu Ile Thr	
440 445 450 455	
g t	
AAG AAT GAG AAT GGA GAA TAC AAC CTC AGC GGC ACT AAG AGG AAC TTC	1506
Lys Asn Glu Asn Gly Glu Tyr Asn Leu Ser Gly Thr Lys Arg Asn Phe	
460 465 470	

FIG.1C

gt	AGT AAC CTT AAG GAC CTT TTG AAT TGC TAC CAG ATG GAA ACT GTG CGC	1554
	Ser Asn Leu Lys Asp Leu Leu Asn Cys Tyr Gln Met Glu Thr Val Arg	
	S 475 480 485	
c	TCA GAC AGT ATC ATC TTC CAG TTT ACC AAA TGC TGC CCC CCA AAG CCA	1602
	Ser Asp Ser Ile Ile Phe Gln Phe Thr Lys Cys Cys Pro Pro Lys Pro	
	490 495 500	
t	AAA GAT AAA TCA AAC CTT CTC GTC TTC AGA ACA AAT GGT ATT TCT GAT	1650
	Lys Asp Lys Ser Asn Leu Leu Val Phe Arg Thr Asn Gly Ile Ser Asp	
	505 510 515 V	
C	GTT CAG ATC TCA CCA ACA TTA CAG AGG CAT AAT AAT GTG AAT CAA ATG	1698
	Val Gln Ile Ser Pro Thr Leu Gln Arg His Asn Asn Val Asn Gln Met	
	520 L 525 530 535	
g	GTG TTT CAC AAA ATC AGG AAT GAA GAT TTA ATA TTT AAT GAA AGT CTT	1746
	Val Phe His Lys Ile Arg Asn Glu Asp Leu Ile Phe Asn Glu Ser Leu	
	540 545 550	
c	GGC CAA GGT ACT TTT ACA AAA ATT TTT AAA GGT GTA AGA AGA GAA GTT	1794
	Gly Gln Gly Thr Phe Thr Lys Ile Phe Lys Gly Val Arg Arg Glu Val	
	555 560 565	
g	GGA GAT TAT GGT CAA CTG CAC AAA ACG GAA GTT CTT TTG AAA GTC CTA	1842
	Gly Asp Tyr Gly Gln Leu His Lys Thr Glu Val Leu Leu Lys Val Leu	
	570 K 575 580	
a	GAT AAA GCA CAT AGG AAC TAT TCA GAG TCT TTC TTC GAA GCA GCA ACC	1890
	Asp Lys Ala His Arg Asn Tyr Ser Glu Ser Phe Phe Glu Ala Ala Ser	
	585 590 595	
a	ATG ATG AGT CAG CTT TCT CAC AAG CAT TTG GTT TTG AAT TAT GGT GTC	1938
	Met Met Ser Gln Leu Ser His Lys His Leu Val Leu Asn Tyr Gly Val	
	600 605 610 615	
t	TGT GTC TGT GGA GAG GAG AAC ATT CTG GTT CAA GAA TTT GTA AAA TTT	1986
	Cys Val Cys Gly Glu Glu Asn Ile Leu Val Gln Glu Phe Val Lys Phe	
	620 625 630	

FIG.1D

GGA TCA CTG GAT ACA TAC CTG AAG AAG AAC AAA AAT TCC ATA AAT ATA Gly Ser Leu Asp Thr Tyr Leu Lys Lys Asn Lys Asn Ser Ile Asn Ile 635 640 645	2034
TTA TGG AAA CTT GGA GTG GCT AAG CAG TTG GCA TGG GCC ATG CAT TTT Leu Trp Lys Leu Gly Val Ala Lys Gln Leu Ala Trp Ala Met His Phe 650 655 660	2082
CTA GAA GAA AAA TCC CTT ATT CAT GGG AAT GTG TGT GCT AAA AAT ATC Leu Glu Glu Lys Ser Leu Ile His Gly Asn Val Cys Ala Lys Asn Ile 665 670 675	2130
CTG CTT ATC AGA GAA GAA GAC AGG AGA ACG GGG AAC CCA CCT TTC ATC Leu Leu Ile Arg Glu Glu Asp Arg Arg Thr Gly Asn Pro Pro Phe Ile 680 685 690 695	2178
AAA CTT AGT GAT CCT GGC ATT AGC ATT ACA GTT CTA CCG AAG GAC ATT Lys Leu Ser Asp Pro Gly Ile Ser Ile Thr Val Leu Pro Lys Asp Ile 700 705 710	2226
CTT CAG GAG AGA ATA CCA TGG GTA CCT CCT GAA TGC ATT GAG AAT CCT Leu Gln Glu Arg Ile Pro Trp Val Pro Pro Glu Cys Ile Glu Asn Pro 715 T 720 725	2274
AAA AAT CTC AAT CTG GCA ACA GAC AAG TGG AGC TTC GGG ACC ACT CTG Lys Asn Leu Asn Leu Ala Thr Asp Lys Trp Ser Phe Gly Thr Thr Leu 730 T 735 740	2322
TGG GAG ATC TGC AGT GGA GGA GAT AAG CCC CTG AGT GCT CTG GAT TCT Trp Glu Ile Cys Ser Gly Gly Asp Lys Pro Leu Ser Ala Leu Asp Ser 745 750 755	2370
CAA AGA AAG CTG CAG TTC TAT GAA GAT AAG CAT CAG CTT CCT GCA CCC Gln Arg Lys Leu Gln Phe Tyr Glu Asp Lys His Gln Leu Pro Ala Pro 760 765 770 775	2418

FIG.1E

9		
AAG TGG ACA GAG TTA GCA AAC CTT ATA AAT AAT TGC ATG GAC TAT GAG	2466	
Lys Trp Thr Glu Leu Ala Asn Leu Ile Asn Asn Cys Met Asp Tyr Glu		
780 785 790		
CCA GAT TTC AGG CCT GCT TTC AGA GCT GTC ATC CGT GAT CTT AAC AGC	2514	
Pro Asp Phe Arg Pro Ala Phe Arg Ala Val Ile Arg Asp Leu Asn Ser		
795 800 805		
CTG TTT ACT CCA GAT TAT GAA CTA CTA ACA GAA AAT GAC ATG CTA CCA	2562	
Leu Phe Thr Pro Asp Tyr Glu Leu Leu Thr Glu Asn Asp Met Leu Pro		
810 815 820		
AAC ATG AGA ATA GGT GCC CTA GGG TTT TCT GGT GCT TTT GAA GAC AGG	2610	
Asn Met Arg Ile Gly Ala Leu Gly Phe Ser Gly Ala Phe Glu Asp Arg		
825 830 835		
GAC CCT ACA CAG TTT GAA GAG AGA CAC TTG AAG TTT CTA CAG CAG CTT	2658	
Asp Pro Thr Gln Phe Glu Glu Arg His Leu Lys Phe Leu Gln Gln Leu		
840 845 850 855		
GGC AAA GGT AAC TTC GGG AGT GTG GAG ATG TGC CGC TAT GAC CCG CTG	2706	
Gly Lys Gly Asn Phe Gly Ser Val Glu Met Cys Arg Tyr Asp Pro Leu		
860 865 870		
CAG GAC AAC ACT GGC GAG GTG GTC GCT GTG AAG AAA CTC CAG CAC AGC	2754	
Gln Asp Asn Thr Gly Glu Val Val Ala Val Lys Lys Leu Gln His Ser		
875 880 885		
ACT GAA GAG CAC CTC CGA GAC TTT GAG AGG GAG ATC GAG ATC CTG AAA	2802	
Thr Glu Glu His Leu Arg Asp Phe Glu Arg Glu Ile Glu Ile Leu Lys		
890 895 900		
TCC TTG CAG CAT GAC AAC ATC GTC AAG TAC AAG GGA GTG TGC TAC AGT	2850	
Ser Leu Gln His Asp Asn Ile Val Lys Tyr Lys Gly Val Cys Tyr Ser		
905 910 915		
CCG GGT CCG CGC AAC CTA AGA TTA ATT ATG GAA TAT TTA CCA TAT GGA	2898	
Ala Gly Arg Arg Asn Leu Arg Leu Ile Met Glu Tyr Leu Pro Tyr Gly		
920 925 930 935		

FIG.1F

AGT TTA CGA GAC TAT CTC CAA AAA CAT AAA GAA CGG ATA GAT CAC AAA Ser Leu Arg Asp Tyr Leu Gln Lys His Lys Glu Arg Ile Asp His Lys 940 945 950	2946
AAA CTT CTT CAA TAC ACA TCT CAG ATA TGC AAG GGC ATG GAA TAT CTT Lys Leu Leu Gln Tyr Thr Ser Gln Ile Cys Lys Gly Met Glu Tyr Leu 955 960 965	2994
GGT ACA AAA AGG TAT ATC CAC AGG GAC CTG GCA ACA AGG AAC ATA TTG Gly Thr Lys Arg Tyr Ile His Arg Asp Leu Ala Thr Arg Asn Ile Leu 970 975 980	3042
GTG GAA AAT GAG AAC AGG GTT AAA ATA GGA GAC TTC GCA TTA ACC AAA Val Glu Asn Glu Asn Arg Val Lys Ile Gly Asp Phe Gly Leu Thr Lys 985 990 995	3090
GTC TTG CCG CAG GAC AAA GAA TAC TAC AAA GTA AAG GAG CCA GGG GAA Val Leu Pro Gln Asp Lys Glu Tyr Tyr Lys Val Lys Glu Pro Gly Glu 1000 1005 1010 1015	3138
AGC CCC ATA TTC TGG TAC GCA CCT GAA TCC TTG ACG GAG AGC AAG TTT Ser Pro Ile Phe Trp Tyr Ala Pro Glu Ser Leu Thr Glu Ser Lys Phe 1020 1025 1030	3186
TCT GTG GCC TCA GAT GTG TGG AGC TTT GGA GTG GTT CTA TAC GAA CTT Ser Val Ala Ser Asp Val Trp Ser Phe Gly Val Val Leu Tyr Glu Leu 1035 1040 1045	3234
TTC ACA TAC ATC GAG AAG AGT AAA AGT CCA CCC GTG GAA TTT ATG CGA Phe Thr Tyr Ile Glu Lys Ser Lys Ser Pro Pro Val Glu Phe Met Arg 1050 1055 1060	3282
ATG ATT GGC AAT GAT AAA CAA GGG CAA ATG ATT GTG TTC CAT TTG ATA Met Ile Gly Asn Asp Lys Gln Gly Gln Met Ile Val Phe His Leu Ile 1065 1070 1075	3330
GAG CTA CTG AAG AGC AAC GGA AGA TTG CCA AGG CCA GAA GGA TGC CCA Glu Leu Leu Lys Ser Asn Gly Arg Leu Pro Arg Pro Glu Gly Cys Pro 1080 1085 1090 1095	3378

FIG.1G

GAT GAG ATT TAT GTG ATC ATG ACA GAG TGC TGG AAC AAC AAT GTG AGC	3426
Asp Glu Ile Tyr Val Ile Met Thr Glu Cys Trp Asn Asn Asn Val Ser	
1100 1105 1110	
c	
CAG CGT CCC TCC TTC AGG GAC CTT TCG TTC GGG TGG ATC AAA TCC GGG	3474
Gln Arg Pro Ser Phe Arg Asp Leu Ser Phe Gly Trp Ile Lys Ser Gly	
1115 1120 1125	
c	
ACA GTA TAGCTGCGTG AAAGACATGG CCTTCACTCA GAGACCAAGC AGACTTCCAG	3530
Thr Val	
c	
AACCAGAACAA AAGCTCTGTA GCCTTGTGTC TACACATCCT TATCATGATG CTAGCTAGGC	3590
(a) (a) (a)	
AGAAGAAACT GTGACGCCGT CTGCTCAAAG CTTTGCTTC	3629

FIG.1H



Human JAK1

ATG GCT TTC TGT GCT AAA ATG AGG AGC TCC AAG AAG ACT GAG GTG AAC	123
Met Ala Phe Cys Ala Lys Met Arg Ser Ser Lys Lys Thr Glu Val Asn	16
CTG GAG GCC CCT GAG CCA GGG GTG GAA GTG ATC TTC TAT CTG TCG GAC	171
Leu Glu Ala Pro Glu Pro Gly Val Glu Val Ile Phe Tyr Leu Ser Asp	32
AGG GAG CCC CTC CGG CTG GGC AGT GGA GAG TAC ACA GCA GAG GAA CTG	219
Arg Glu Pro Leu Arg Leu Gly Ser Gly Glu Tyr Thr Ala Glu Glu Leu	48
TGC ATC AGG GCT GCA CAG GCA TGC CGT ATC TCT CCT CTT TGT CAC AAC	267
Cys Ile Arg Ala Ala Gln Ala Cys Arg Ile Ser Pro Leu Cys His Asn	64
CTC TTT GCC CTG TAT GAC GAG AAC ACC AAG CTC TGG TAT GCT CCA AAT	315
Leu Phe Ala Leu Tyr Asp Glu Asn Thr Lys Leu Trp Tyr Ala Pro Asn	80
CGC ACC ATC ACC GTT GAT GAC AAG ATG TCC CTC CGG CTC CAC TAC CGG	363
Arg Thr Ile Thr Val Asp Asp Lys Met Ser Leu Arg Leu His Tyr Arg	96
ATG AGG TTC TAT TTC ACC AAT TGG CAT GGA ACC AAC GAC AAT GAG CAG	411
Met Arg Phe Tyr Phe Thr Asn Trp His Gly Thr Asn Asp Asn Glu Gln	112
TCA GTG TGG CGT CAT TCT CCA AAG AAG CAG AAA AAT GGC TAC GAG AAA	459
Ser Val Trp Arg His Ser Pro Lys Lys Gln Lys Asn Gly Tyr Glu Lys	128
AAA AAG ATT CCA GAT GCA ACC CCT CTC CTT GAT GCC AGC TCA CTG GAG	507
Lys Lys Ile Pro Asp Ala Thr Pro Leu Leu Asp Ala Ser Ser Leu Glu	144
TAT CTG TTT GCT CAG GGA CAG TAT GAT TTG GTG AAA TGC CTG GCT CCT	555
Tyr Leu Phe Ala Gln Gly Gln Tyr Asp Leu Val Lys Cys Leu Ala Pro	160
ATT CGA GAC CCC AAG ACC GAG CAG GAT GGA CAT GAT ATT GAG AAC GAG	603
Ile Arg Asp Pro Lys Thr Glu Gln Asp Gly His Asp Ile Glu Asn Glu	176
TGT CTA GGG ATG GCT GTC CTG GCC ATC TCA CAC TAT GCC ATG ATG AAG	651
Cys Leu Gly Met Ala Val Leu Ala Ile Ser His Tyr Ala Met Met Lys	192
AAG ATG CAG TTG CCA GAA CTG CCC AAG GAC ATC AGC TAC AAG CGA TAT	699
Lys Met Gln Leu Pro Glu Leu Pro Lys Asp Ile Ser Tyr Lys Arg Tyr	208
ATT CCA GAA ACA TTG AAT AAG TCC ATC AGA CAG AGG AAC CTT CTC ACC	747
Ile Pro Glu Thr Leu Asn Lys Ser Ile Arg Gln Arg Asn Leu Leu Thr	224
AGG ATG CGG ATA AAT AAT GTT TTC AAG GAT TTC CTA AAG GAA TTT AAC	795
Arg Met Arg Ile Asn Asn Val Phe Lys Asp Phe Leu Lys Glu Phe Asn	240
AAC AAG ACC ATT TGT GAC AGC AGC GTG TCC ACG CAT GAC CTG AAG GTG	843
Asn Lys Thr Ile Cys Asp Ser Ser Val Ser Thr His Asp Leu Lys Val	256
AAA TAC TTG GCT ACC TTG GAA ACT TTG ACA AAA CAT TAC GGT GCT GAA	891
Lys Tyr Leu Ala Thr Leu Glu Thr Leu Thr Lys His Tyr Gly Ala Glu	272

FIG.2A

ATA TTT GAG ACT TCC ATG TTA CTG ATT TCA TCA GAA AAT GAG ATG AAT	939
Ile Phe Glu Thr Ser Met Leu Leu Ile Ser Ser Glu Asn Glu Met Asn	288
TGG TTT CAT TCG AAT GAC GGT GGA AAC GTT CTC TAC TAC GAA GTG ATG	987
Trp Phe His Ser Asn Asp Gly Gly Asn Val Leu Tyr Tyr Glu Val Met	304
GTG ACT GGG AAT CTT GGA ATC CAG TGG AGG CAT AAA CCA AAT GTT GTT	1035
Val Thr Gly Asn Leu Gly Ile Gln Trp Arg His Lys Pro Asn Val Val	320
TCT GTT GAA AAG GAA AAA AAT AAA CTG AAG CGG AAA AAA CTG GAA AAT	1083
Ser Val Glu Lys Glu Lys Asn Lys Leu Lys Arg Lys Lys Leu Glu Asn	336
AAA GAC AAG AAG GAT GAG GAG AAA AAC AAG ATC CGG GAA GAG TGG AAC	1131
Lys Asp Lys Lys Asp Glu Glu Lys Asn Lys Ile Arg Glu Glu Trp Asn	352
AAT TTT TCA TTC TTC CCT GAA ATC ACT CAC ATT GTA ATA AAG GAG TCT	1179
Asn Phe Ser Phe Phe Pro Glu Ile Thr His Ile Val Ile Lys Glu Ser	368
GTG GTC AGC ATT AAC AAG CAG GAC AAC AAG AAA ATG GAA CTG AAG CTC	1227
Val Val Ser Ile Asn Lys Gln Asp Asn Lys Lys Met Glu Leu Lys Leu	384
TCT TCC CAC GAG GAG GCC TTG TCC TTT GTG TCC CTG GTA GAT GGC TAC	1275
Ser Ser His Glu Glu Ala Leu Ser Phe Val Ser Leu Val Asp Gly Tyr	400
TTC CGG CTC ACA GCA GAT GCC CAT CAT TAC CTC TGC ACC GAC GTG GCC	1323
Phe Arg Leu Thr Ala Asp Ala His His Tyr Leu Cys Thr Asp Val Ala	416
CCC CCG TTG ATC GTC CAC AAC ATA CAG AAT GGC TGT CAT GGT CCA ATC	1371
Pro Pro Leu Ile Val His Asn Ile Gln Asn Gly Cys His Gly Pro Ile	432
TGT ACA GAA TAC GCC ATC AAT AAA TTG CGG CAA GAA GGA AGC GAG GAG	1419
Cys Thr Glu Tyr Ala Ile Asn Lys Leu Arg Gln Glu Gly Ser Glu Glu	448
GGG ATG TAC GTG CTG AGG TGG AGC TGC ACC GAC TTT GAC AAC ATC CTC	1467
Gly Met Tyr Val Leu Arg Trp Ser Cys Thr Asp Phe Asp Asn Ile Leu	464
ATG ACC GTC ACC TGC TTT GAG AAG TCT GAG CAG GTG CAG GGT GCC CAG	1515
Met Thr Val Thr Cys Phe Glu Lys Ser Glu Gln Val Gln Gly Ala Gln	480
AAG CAG TTC AAG AAC TTT CAG ATC GAG GTG CAG AAG GGC CGC TAC AGT	1563
Lys Gln Phe Lys Asn Phe Gln Ile Glu Val Gln Lys Gly Arg Tyr Ser	496
CTG CAC GGT TCG GAC CGC AGC TTC CCC AGC TTG GGA GAC CTC ATG AGC	1611
Leu His Gly Ser Asp Arg Ser Phe Pro Ser Leu Gly Asp Leu Met Ser	512
CAC CTC AAG AAG CAG ATC CTG CGC ACG GAT AAC ATC AGC TTC ATG CTA	1659
His Leu Lys Lys Gln Ile Leu Arg Thr Asp Asn Ile Ser Phe Met Leu	528
AAA CGC TGC TGC CAG CCC AAG CCC CGA GAA ATC TCC AAC CTG CTG GTG	1707
Lys Arg Cys Cys Gln Pro Lys Pro Arg Glu Ile Ser Asn Leu Leu Val	544
GCT ACT AAG AAA GCC CAG GAG TGG CAG CCC GTC TAC CCC ATG AGC CAG	1755
Ala Thr Lys Lys Ala Gln Glu Trp Gln Pro Val Tyr Pro Met Ser Gln	560

FIG.2B

CTG AGT TTC GAT CGG ATC CTC AAG AAG GAT CTG GTG CAG GGC GAG CAC	1803
Leu Ser Phe Asp Arg Ile Leu Lys Lys Asp Leu Val Gln Gly Glu His	576
CTT GGG AGA GGC ACG AGA ACA CAC ATC TAT TCT GGG ACC CTG ATG GAT	1851
Leu Gly Arg Gly Thr Arg Thr His Ile Tyr Ser Gly Thr Leu Met Asp	592
TAC AAG GAT GAC GAA GGA ACT TCT GAA GAG AAG AAG ATA AAA GTG ATC	1899
Tyr Lys Asp Asp Glu Gly Thr Ser Glu Glu Lys Lys Ile Lys Val Ile	608
CTC AAA GTC TTA GAC CCC AGC CAC AGG GAT ATT TCC CTG GCC TTC TTC	1947
Leu Lys Val Leu Asp Pro Ser His Arg Asp Ile Ser Leu Ala Phe Phe	624
GAG GCA GCC AGC ATG ATG AGA CAG GTC TCC CAC AAA CAC ATC GTG TAC	1995
Glu Ala Ala Ser Met Met Arg Gln Val Ser His Lys His Ile Val Tyr	640
CTC TAT GGC GTC TGT GTC CGC GAC GTG GAG AAT ATC ATG GTG GAA GAG	2043
Leu Tyr Gly Val Cys Val Arg Asp Val Glu Asn Ile Met Val Glu Glu	656
TTT GTG GAA GGG GGT CCT CTG GAT CTC TTC ATG CAC CGG AAA AGT GAT	2091
Phe Val Glu Gly Gly Pro Leu Asp Leu Phe Met His Arg Lys Ser Asp	672
GTC CTT ACC ACA CCA TGG AAA TTC AAA GTT GCC AAA CAG CTG GCC AGT	2139
Val Leu Thr Thr Pro Trp Lys Phe Lys Val Ala Lys Gln Leu Ala Ser	688
GCC CTG AGC TAC TTG GAG GAT AAA GAC CTG GTC CAT GGA AAT GTG TGT	2187
Ala Leu Ser Tyr Leu Glu Asp Lys Asp Leu Val His Gly Asn Val Cys	704
ACT AAA AAC CTC CTC CTG GCC CGT GAG GGA ATC GAC AGT GAG TGT GGC	2235
Thr Lys Asn Leu Leu Leu Ala Arg Glu Gly Ile Asp Ser Glu Cys Gly	720
CCA TTC ATC AAG CTC AGT GAC CCC GGC ATC CCC ATT ACG GTG CTG TCT	2283
Pro Phe Ile Lys Leu Ser Asp Pro Gly Ile Pro Ile Thr Val Leu Ser	736
AGG CAA GAA TGC ATT GAA CGA ATC CCA TGG ATT GCT CCT GAG TGT GTT	2331
Arg Gln Glu Cys Ile Glu Arg Ile Pro Trp Ile Ala Pro Glu Cys Val	752
GAG GAC TCC AAG AAC CTG AGT GTG GCT GCT GAC AAG TGG AGC TTT GGA	2379
Glu Asp Ser Lys Asn Leu Ser Val Ala Ala Asp Lys Trp Ser Phe Gly	768
ACC ACG CTC TGG GAA ATC TGC TAC AAT GGC GAG ATC CCC TTG AAA GAC	2427
Thr Thr Leu Trp Glu Ile Cys Tyr Asn Gly Glu Ile Pro Leu Lys Asp	784
AAG ACG CTG ATT GAG AAA GAG AGA TTC TAT GAA AGC CGG TGC AGG CCA	2475
Lys Thr Leu Ile Glu Lys Glu Arg Phe Tyr Glu Ser Arg Cys Arg Pro	800
GTG ACA CCA TCA TGT AAG GAG CTG GCT GAC CTC ATG ACC CGC TGC ATG	2523
Val Thr Pro Ser Cys Lys Glu Leu Ala Asp Leu Met Thr Arg Cys Met	816
AAC TAT GAC CCC AAT CAG AGG CCT TTC TTC CGA GCC ATC ATG AGA GAC	2571
Asn Tyr Asp Pro Asn Gln Arg Pro Phe Phe Arg Ala Ile Met Arg Asp	832
ATT AAT AAG CTT GAA GAG CAG AAT CCA GAT ATT GTT TCC AGA AAA AAA	2619
Ile Asn Lys Leu Glu Glu Gln Asn Pro Asp Ile Val Ser Arg Lys Lys	848

FIG.2C

AAC CAG CCA ACT GAA GTG GAC CCC ACA CAT TTT GAG AAG CGC TTC CTA	2667
Asn Gln Pro Thr Glu Val Asp Pro Thr His Phe Glu Lys Arg Phe Leu	864
AAG AGG ATC CGT GAC TTG CGA GAG GGC CAC TTT GGG AAG GTT GAG CTC	2715
Lys Arg Ile Arg Asp Leu Gly Glu Gly His Phe Gly Lys Val Glu Leu	880
TGC AGG TAT GAC CCC GAA GAC AAT ACA GGG GAG CAG GTG GCT GTT AAA	2763
Cys Arg Tyr Asp Pro Glu Asp Asn Thr Gly Glu Gln Val Ala Val Lys	896
TCT CTG AAG CCT GAG AGT GGA GGT AAC CAC ATA GCT GAT CTG AAA AAG	2811
Ser Leu Lys Pro Glu Ser Gly Gly Asn His Ile Ala Asp Leu Lys Lys	912
GAA ATC GAG ATC TTA AGG AAC CTC TAT CAT GAG AAC ATT GTG AAG TAC	2859
Glu Ile Glu Ile Leu Arg Asn Leu Tyr His Glu Asn Ile Val Lys Tyr	928
AAA GGA ATC TGC ACA GAA GAC GGA GGA AAT GGT ATT AAG CTC ATC ATG	2907
Lys Gly Ile Cys Thr Glu Asp Gly Gly Asn Gly Ile Lys Leu Ile Met	944
GAA TTT CTG CCT TCG GGA AGC CTT AAG GAA TAT CTT CCA AAG AAT AAG	2955
Glu Phe Leu Pro Ser Gly Ser Leu Lys Glu Tyr Leu Pro Lys Asn Lys	960
AAC AAA ATA AAC CTC AAA CAG CAG CTA AAA TAT GCC GTT CAG ATT TGT	3003
Asn Lys Ile Asn Leu Lys Gln Gln Leu Lys Tyr Ala Val Gln Ile Cys	976
AAG GGG ATG GAC TAT TTG GGT TCT CGG CAA TAC GTT CAC CGG GAC TTG	3051
Lys Gly Met Asp Tyr Leu Gly Ser Arg Gln Tyr Val His Arg Asp Leu	992
GCA GCA AGA AAT GTC CTT GTT GAG AGT GAA CAC CAA GTG AAA ATT GGA	3099
Ala Ala Arg Asn Val Leu Val Glu Ser Glu His Gln Val Lys Ile Gly	1008
GAC TTC GGT TTA ACC AAA GCA ATT GAA ACC GAT AAG GAG TAT TAC ACC	3147
Asp Phe Gly Leu Thr Lys Ala Ile Glu Thr Asp Lys Glu Tyr Tyr Thr	1024
GTC AAG GAT GAC CGG GAC AGC CCT GTG TTT TGG TAT GCT CCA GAA TGT	3195
Val Lys Asp Asp Arg Asp Ser Pro Val Phe Trp Tyr Ala Pro Glu Cys	1040
TTA ATG CAA TCT AAA TTT TAT ATT GCC TCT GAC GTC TGG TCT TTT GGA	3243
Leu Met Gln Ser Lys Phe Tyr Ile Ala Ser Asp Val Trp Ser Phe Gly	1056
GTC ACT CTG CAT GAG CTG CTG ACT TAC TGT GAT TCA GAT TCT AGT CCC	3291
Val Thr Leu His Glu Leu Leu Thr Tyr Cys Asp Ser Asp Ser Ser Pro	1072
ATG GCT TTG TTC CTG AAA ATG ATA GGC CCA ACC CAT GGC CAG ATG ACA	3339
Met Ala Leu Phe Leu Lys Met Ile Gly Pro Thr His Gly Gln Met Thr	1088
GTC ACA AGA CTT GTG AAT ACG TTA AAA GAA GGA AAA CGC CTG CCG TGC	3387
Val Thr Arg Leu Val Asn Thr Leu Lys Glu Gly Lys Arg Leu Pro Cys	1104
CCA CCT AAC TGT CCA GAT GAG GTT TAT CAG CTT ATG AGA AAA TGC TGG	3435
Pro Pro Asn Cys Pro Asp Glu Val Tyr Gln Leu Met Arg Lys Cys Trp	1120
GAA TTC CAA CCA TCC AAT CGG ACA AGC TTT CAG AAC CTT ATT GAA GGA	3483
Glu Phe Gln Pro Ser Asn Arg Thr Ser Phe Gln Asn Leu Ile Glu Gly	1136
TTT GAA GCA CTT TTA AAA TAA	3504
Phe Glu Ala Leu Leu Lys *	1143

FIG.2D

# Human TYK2

ATG CCT CTG CGC CAC TGG GGG ATG GCC AGG GGC AGT AAG CCC GTT GGG	354
Met Pro Leu Arg His Trp Gly Met Ala Arg Gly Ser Lys Pro Val Gly	16
GAT GGA GCC CAG CCC ATG GCT GCC ATG GGA GGC CTG AAG GTG CTT CTG	402
Asp Gly Ala Gln Pro Met Ala Ala Met Gly Gly Leu Lys Val Leu Leu	32
CAC TGG GCT GGT CCA GGC GGC GGG GAG CCC TGG GTC ACT TTC AGT GAG	450
His Trp Ala Gly Pro Gly Gly Gly Glu Pro Trp Val Thr Phe Ser Glu	48
TCA TCG CTG ACA GCT GAG GAA GTC TGC ATC CAC ATT GCA CAT AAA GTT	498
Ser Ser Leu Thr Ala Glu Glu Val Cys Ile His Ile Ala His Lys Val	64
GGT ATC ACT CCT CCT TGC TTC AAT CTC TTT GCC CTC TTC GAT GCT CAG	546
Gly Ile Thr Pro Pro Cys Phe Asn Leu Phe Ala Leu Phe Asp Ala Gln	80
GCC CAA GTC TGG TTG CCC CCA AAC CAC ATC CTA GAG ATC CCC AGA GAT	594
Ala Gln Val Trp Leu Pro Pro Asn His Ile Leu Glu Ile Pro Arg Asp	96
GCA AGC CTG ATG CTA TAT TTC CGC ATA AGG TTT TAT TTC CGG AAC TGG	642
Ala Ser Leu Met Leu Tyr Phe Arg Ile Arg Phe Tyr Phe Arg Asn Trp	112
CAT GGC ATG AAT CCT CGG GAA CCG GCT GTG TAC CGT TGT GGG CCC CCA	690
His Gly Met Asn Pro Arg Glu Pro Ala Val Tyr Arg Cys Gly Pro Pro	128
GGA ACC GAG GCA TCC TCA GAT CAG ACA GCA CAG GGG ATG CAA CTC CTG	738
Gly Thr Glu Ala Ser Ser Asp Gln Thr Ala Gln Gly Met Gln Leu Leu	144
GAC CCA GCC TCA TTT GAG TAC CTC TTT GAG CAG GGC AAG CAT GAG TTT	786
Asp Pro Ala Ser Phe Glu Tyr Leu Phe Glu Gln Gly Lys His Glu Phe	160
GTG AAT GAC GTG GCA TCA CTG TGG GAG CTG TCG ACC GAG GAG GAG ATC	834
Val Asn Asp Val Ala Ser Leu Trp Glu Leu Ser Thr Glu Glu Glu Ile	176
CAC CAC TTT AAG AAT GAG AGC CTG GGC ATG GCC TTT CTG CAC CTC TGT	882
His His Phe Lys Asn Glu Ser Leu Gly Met Ala Phe Leu His Leu Cys	192
CAC CTC GCT CTC CGC CAT GGC ATC CCC CTG GAG GAG GTG GCC AAG AAG	930
His Leu Ala Leu Arg His Gly Ile Pro Leu Glu Glu Val Ala Lys Lys	208
ACC AGC TTC AAG GAC TGC ATC CCG CGC TCC TTC CGC CGG CAT ATC CCG	978
Thr Ser Phe Lys Asp Cys Ile Pro Arg Ser Phe Arg Arg His Ile Arg	224
CAG CAC AGC GCC CTG ACC CGG CTG CGC CTT CGG AAC GTC TTC CGC AGG	1026
Gln His Ser Ala Leu Thr Arg Leu Arg Leu Arg Asn Val Phe Arg Arg	240
TTC CTG CGG GAC TTC CAG CCG GGC CGA CTC TCC CAG CAG ATG GTC ATG	1074
Phe Leu Arg Asp Phe Gln Pro Gly Arg Leu Ser Gln Gln Met Val Met	256
GTC AAA TAC CTA GCC ACA CTC GAG CGG CTG GCA CCC CGC TTC GGC ACA	1122
Val Lys Tyr Leu Ala Thr Leu Glu Arg Leu Ala Pro Arg Phe Gly Thr	272

FIG.3A

GAG CGT GTG CCC GTG TGC CAC CTG AGG CTG CTG GCC CAG GCC GAG GGG	1170
Glu Arg Val Pro Val Cys His Leu Arg Leu Leu Ala Gln Ala Glu Gly	288
GAG CCC TGC TAC ATC CCG GAC AGT GGG GTG GCC CCT ACA GAC CCT GGC	1218
Glu Pro Cys Tyr Ile Arg Asp Ser Gly Val Ala Pro Thr Asp Pro Gly	304
CCT GAG TCT GCT GCT GGG CCC CCA ACC CAC GAG GTG CTG GTG ACA GGC	1266
Pro Glu Ser Ala Ala Gly Pro Pro Thr His Glu Val Leu Val Thr Gly	320
ACT GGT GGC ATC CAG TGG TGG CCA GTA GAG GAG GAG GTG AAC AAG GAG	1314
Thr Gly Gly Ile Gln Trp Trp Pro Val Glu Glu Glu Val Asn Lys Glu	336
GAG GGT TCT AGT GGC AGC AGT GGC AGG AAC CCC CAA GCC AGC CTG TTT	1362
Glu Gly Ser Ser Gly Ser Ser Gly Arg Asn Pro Gln Ala Ser Leu Phe	352
GGG AAG AAG GCC AAG GCT CAC AAG GCA TTC GGC CAG CCG GCA GAC AGG	1410
Gly Lys Lys Ala Lys Ala His Lys Ala Phe Gly Gln Pro Ala Asp Arg	368
CCG CCG GAG CCA CTG TGG GCC TAC TTC TGT GAC TTC CCG GAC ATC ACC	1458
Pro Arg Glu Pro Leu Trp Ala Tyr Phe Cys Asp Phe Arg Asp Ile Thr	384
CAC GTG GTG CTG AAA GAG CAC TGT GTC AGC ATC CAC CCG CAG GAC AAC	1506
His Val Val Leu Lys Glu His Cys Val Ser Ile His Arg Gln Asp Asn	400
AAG TGC CTG GAG CTG AGC TTG CCT TCC CCG GCT GCG GCG CTG TCC TTC	1554
Lys Cys Leu Glu Leu Ser Leu Pro Ser Arg Ala Ala Ala Leu Ser Phe	416
GTG TCG CTG GTG GAC GGC TAT TTC CCG CTG ACG GCC GAC TCC AGC CAC	1602
Val Ser Leu Val Asp Gly Tyr Phe Arg Leu Thr Ala Asp Ser Ser His	432
TAC CTG TGC CAC GAG GTG GCT CCC CCA CCG CTG GTG ATG AGC ATC CCG	1650
Tyr Leu Cys His Glu Val Ala Pro Pro Arg Leu Val Met Ser Ile Arg	448
GAT GGG ATC CAC GGA CCC CTG CTG GAG CCA TTT GTG CAG GCC AAG CTG	1698
Asp Gly Ile His Gly Pro Leu Leu Glu Pro Phe Val Gln Ala Lys Leu	464
CGG CCC GAG GAC GGC CTG TAC CTC ATT CAC TGG AGC ACC AGC CAC CCC	1746
Arg Pro Glu Asp Gly Leu Tyr Leu Ile His Trp Ser Thr Ser His Pro	480
TAC CCG CTG ATC CTC ACA GTG GCC CAG CGT AGC CAG GCA CCA GAC GGC	1794
Tyr Arg Leu Ile Leu Thr Val Ala Gln Arg Ser Gln Ala Pro Asp Gly	496
ATG CAG AGC TTG CCG CTC CGA AAG TTC CCC ATT GAG CAG CAG GAC GGC	1842
Met Gln Ser Leu Arg Leu Arg Lys Phe Pro Ile Glu Gln Gln Asp Gly	512
GCC TTC GTG CTG GAG GGC TGG GGC CCG TCC TTC CCC AGC GTT CCG GAA	1890
Ala Phe Val Leu Glu Gly Trp Gly Arg Ser Phe Pro Ser Val Arg Glu	528
CTT GGG GCT GCC TTG CAG GGC TGC TTG CTG AGG GCC GGG GAT GAC TGC	1938
Leu Gly Ala Ala Leu Gln Gly Cys Leu Leu Arg Ala Gly Asp Asp Cys	544
TTC TCT CTG CGT CCG TGT TGC CTG CCC CAA CCA GGA GAA ACC TCC AAT	1986
Phe Ser Leu Arg Arg Cys Cys Leu Pro Gln Pro Gly Glu Thr Ser Asn	560

FIG.3B

CTC ATC ATC ATG CGG GGG GCT CGG GCC AGC CCC AGG ACA CTC AAC CTC	2034
Leu Ile Ile Met Arg Gly Ala Arg Ala Ser Pro Arg Thr Leu Asn Leu	576
AGC CAG CTC AGC TTC CAC CGG GTT GAC CAG AAG GAG ATC ACC CAG CTG	2082
Ser Gln Leu Ser Phe His Arg Val Asp Gln Lys Glu Ile Thr Gln Leu	592
TCC CAC TTG GGC CAG GGC ACA AGG ACC AAC GTG TAT GAG GGC CGC CTG	2130
Ser His Leu Gly Gln Gly Thr Arg Thr Asn Val Tyr Glu Gly Arg Leu	608
CGA GTG GAG GGC AGC GGG GAC CCT GAG GAG GGC AAG ATG GAT GAC GAG	2178
Arg Val Glu Gly Ser Gly Asp Pro Glu Glu Gly Lys Met Asp Asp Glu	624
GAC CCC CTC GTG CCT GGC AGG GAC CGT GGG CAG GAG CTA CGA GTG GTG	2226
Asp Pro Leu Val Pro Gly Arg Asp Arg Gly Gln Glu Leu Arg Val Val	640
CTC AAA GTG CTG GAC CCT AGT CAC CAT GAC ATC GCC CTG GCC TTC TAC	2274
Leu Lys Val Leu Asp Pro Ser His His Asp Ile Ala Leu Ala Phe Tyr	656
GAG ACA GCC AGC CTC ATG AGC CAG GTC TCC CAC ACG CAC CTG GCC TTC	2322
Glu Thr Ala Ser Leu Met Ser Gln Val Ser His Thr His Leu Ala Phe	672
GTG CAT GGC GTC TGT GTG CGC GGC CCT GAA AAT AGC ATG GTG ACA GAG	2370
Val His Gly Val Cys Val Arg Gly Pro Glu Asn Ser Met Val Thr Glu	688
TAC GTG GAG CAC GGA CCC CTG GAT GTG TGG CTG CGG AGG GAG CGG GGC	2418
Tyr Val Glu His Gly Pro Leu Asp Val Trp Leu Arg Arg Glu Arg Gly	704
CAT GTG CCC ATG GCT TGG AAG ATG GTG GTG GCC CAG CAG CTG GCC AGC	2466
His Val Pro Met Ala Trp Lys Met Val Val Ala Gln Gln Leu Ala Ser	720
GCC CTC AGC TAC CTG GAG AAC AAG AAC CTG GTT CAT GGT AAT GTG TGT	2514
Ala Leu Ser Tyr Leu Glu Asn Lys Asn Leu Val His Gly Asn Val Cys	736
GGC CGG AAC ATC CTG CTG GCC CGG CTG GGG TTG GCA GAG GGC ACC AGC	2562
Gly Arg Asn Ile Leu Leu Ala Arg Leu Gly Leu Ala Glu Gly Thr Ser	752
CCC TTC ATC AAG CTG AGT GAT CCT GGC GTG GGC CTG GGC GCC CTC TCC	2610
Pro Phe Ile Lys Leu Ser Asp Pro Gly Val Gly Leu Gly Ala Leu Ser	768
AGG GAG GAG CGG GTG GAG AGG ATC CCC TGG CTG GCC CCC GAA TGC CTA	2658
Arg Glu Glu Arg Val Glu Arg Ile Pro Trp Leu Ala Pro Glu Cys Leu	784
CCA GGT GGG GCC AAC AGC CTA AGC ACC GCC ATG GAC AAG TGG GGG TTT	2706
Pro Gly Gly Ala Asn Ser Leu Ser Thr Ala Met Asp Lys Trp Gly Phe	800
GGC GCC ACC CTC CTG GAG ATC TGC TTT GAC GGA GAG GCC CCT CTG CAG	2754
Gly Ala Thr Leu Leu Glu Ile Cys Phe Asp Gly Glu Ala Pro Leu Gln	816
AGC CGC AGT CCC TCC GAG AAG GAG CAT TTC TAC CAG AGG CAG CAC CGG	2802
Ser Arg Ser Pro Ser Glu Lys Glu His Phe Tyr Gln Arg Gln His Arg	832
CTG CCC GAG CCC TCC TGC CCA CAG CTG GCC ACA CTC ACC AGC CAG TGT	2850
Leu Pro Glu Pro Ser Cys Pro Gln Leu Ala Thr Leu Thr Ser Gln Cys	848

FIG.3C

CTG ACC TAT GAG CCA ACC CAG AGG CCA TCA TTC CGC ACC ATC CTG CGT	2898
Leu Thr Tyr Glu Pro Thr Gln Arg Pro Ser Phe Arg Thr Ile Leu Arg	864
GAC CTC ACC CGC GTG CAG CCC CAC AAT CTT GCT GAC GTC TTG ACT GTG	2946
Asp Leu Thr Arg Val Gln Pro His Asn Leu Ala Asp Val Leu Thr Val	880
AAC CGG GAC TCA CCG GCC GTC GGA CCT ACT ACT TTC CAC AAG CGC TAT	2994
Asn Arg Asp Ser Pro Ala Val Gly Pro Thr Thr Phe His Lys Arg Tyr	896
TTG AAA AAG ATC CGA GAT CTG GGC GAG GGT CAC TTC GGC AAG GTC AGC	3042
Leu Lys Lys Ile Arg Asp Leu Gly Glu Gly His Phe Gly Lys Val Ser	912
TTG TAC TGC TAC GAT CCG ACC AAC GAC GGC ACT GGC GAG ATG GTG GCG	3090
Leu Tyr Cys Tyr Asp Pro Thr Asn Asp Gly Thr Gly Glu Met Val Ala	928
GTG AAA GCC CTC AAG GCA GAC TGC GGC CCC CAG CAC CGC TCG GGC TGG	3138
Val Lys Ala Leu Lys Ala Asp Cys Gly Pro Gln His Arg Ser Gly Trp	944
AAG CAG GAG ATT GAC ATT CTG CGC ACG CTC TAC CAC GAG CAC ATC ATC	3186
Lys Gln Glu Ile Asp Ile Leu Arg Thr Leu Tyr His Glu His Ile Ile	960
AAG TAC AAG GGC TGC TGC GAG GAC CAA GGC GAG AAG TCG CTG CAG CTG	3234
Lys Tyr Lys Gly Cys Cys Glu Asp Gln Gly Glu Lys Ser Leu Gln Leu	976
GTC ATG GAG TAC GTG CCC CTG GGC AGC CTC CGA GAC TAC CTG CCC CGG	3282
Val Met Glu Tyr Val Pro Leu Gly Ser Leu Arg Asp Tyr Leu Pro Arg	992
CAC AGC ATC GGG CTG GCC CAG CTG CTG CTC TTC GCC CAG CAG ATC TGC	3330
His Ser Ile Gly Leu Ala Gln Leu Leu Leu Phe Ala Gln Gln Ile Cys	1008
GAG GGC ATG GCC TAT CTG CAC GCG CAC GAC TAC ATC CAC CGA GAC CTA	3378
Glu Gly Met Ala Tyr Leu His Ala His Asp Tyr Ile His Arg Asp Leu	1024
GCC GCG CGC AAC GTG CTG CTG GAC AAC GAC AGG CTG GTC AAG ATC GGG	3426
Ala Ala Arg Asn Val Leu Leu Asp Asn Asp Arg Leu Val Lys Ile Gly	1040
GAC TTT GGC CTA GCC AAG GCC GTG CCC GAA GGC CAC GAG TAC TAC CGC	3474
Asp Phe Gly Leu Ala Lys Ala Val Pro Glu Gly His Glu Tyr Tyr Arg	1056
GTG CGC GAG GAT GGG GAC AGC CCC GTG TTC TGG TAT GCC CCA GAG TGC	3522
Val Arg Glu Asp Gly Asp Ser Pro Val Phe Trp Tyr Ala Pro Glu Cys	1072
CTG AAG GAG TAT AAG TTC TAC TAT GCG TCA GAT GTC TGG TCC TTC GGG	3570
Leu Lys Glu Tyr Lys Phe Tyr Tyr Ala Ser Asp Val Trp Ser Phe Gly	1088
GTG ACC CTG TAT GAG CTG CTG ACG CAC TGT GAC TCC AGC CAG AGC CCC	3618
Val Thr Leu Tyr Glu Leu Leu Thr His Cys Asp Ser Ser Gln Ser Pro	1104
CCC ACG AAA TTC CTT GAG CTC ATA GGC ATT GCT CAG GGT CAG ATG ACA	3666
Pro Thr Lys Phe Leu Glu Leu Ile Gly Ile Ala Gln Gly Gln Met Thr	1120
GTT CTG AGA CTC ACT GAG TTG CTG GAA CGA GGG GAG AGG CTG CCA CGG	3714
Val Leu Arg Leu Thr Glu Leu Leu Glu Arg Gly Glu Arg Leu Pro Arg	1136

FIG.3D



CCC GAC AAA TGT CCC TGT GAG GTC TAT CAT CTC ATG AAG AAC TGC TGG	3762
Pro Asp Lys Cys Pro Cys Glu Val Tyr His Leu Met Lys Asn Cys Trp	1152
GAG ACA GAG GCG TCC TTT CGC CCA ACC TTC GAG AAC CTC ATA CCC ATT	3810
Glu Thr Glu Ala Ser Phe Arg Pro Thr Phe Glu Asn Leu Ile Pro Ile	1168
CTG AAG ACA GTC CAT GAG AAG TAC CAA GGC CAG GCC CCT TCA GTG TTC	3858
Leu Lys Thr Val His Glu Lys Tyr Gln Gly Gln Ala Pro Ser Val Phe	1184
AGC GTG TGC	3867
Ser Val Cys	1187

FIG.3E

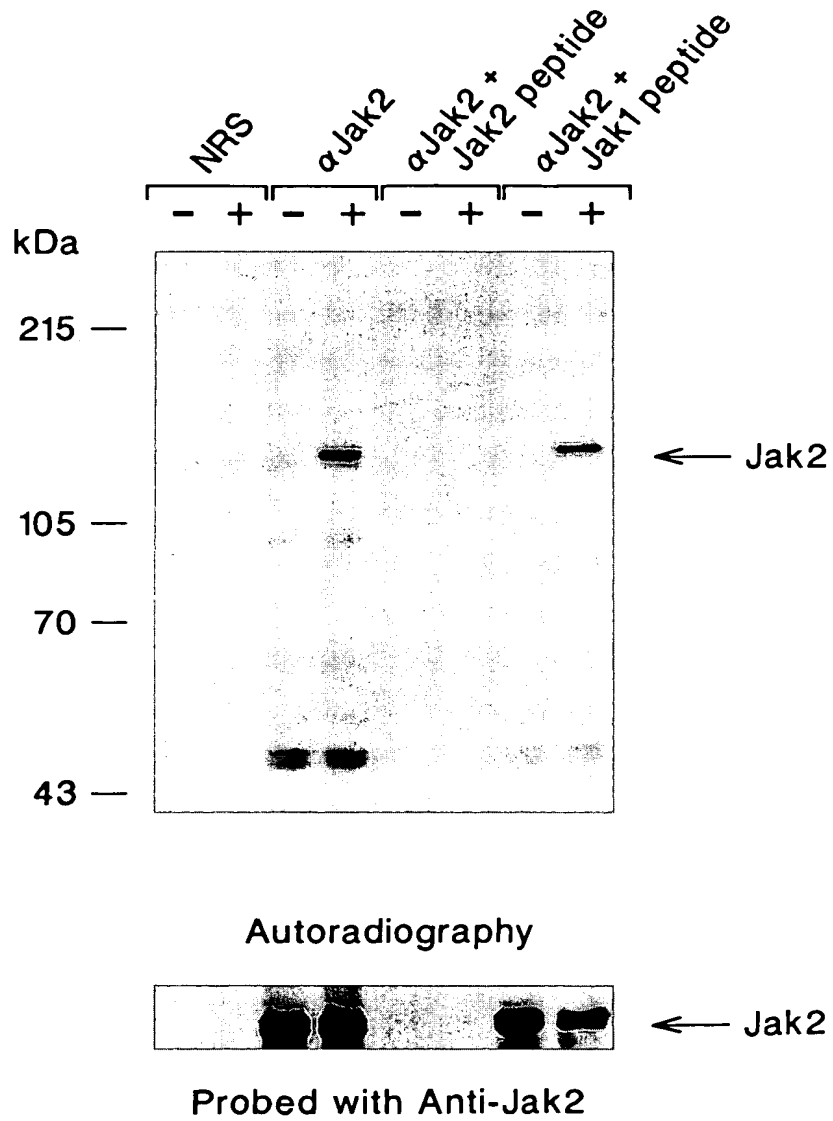


FIG.4

pileup.msf(Jak1)	..MQYLNKE	DCNAMAFCAK	MRSFKKTEVK	QVVP.EPGVE	VTFYLLDREP
pileup.msf(Tyk2)	MPLRHGGMAR	GSKPVG....	.....DGAQ	PMAA.MGGLK	VLLHWAGPGG
pileup.msf(Jak2)	MGMACLTMTTE	MEATSTSPVH	QNGDIPGSAN	SVKQIEPVLQ	VLYYHSLGQA
Consensus	M-M--L-M-E	-----	-----A-	-V---EPGL-	V-LY-----
pileup.msf(Jak1)	....LRLGSG	EYTAEELCIR	AAQECISISPL	CHNLFALYDE	STKLWYAPNR
pileup.msf(Tyk2)	GEPWVTFSES	SLTAEVVCIH	IAHKVGITPP	CFNLFALFDA	QAQVWLPNNH
pileup.msf(Jak2)	EGEYLFPSG	EYVAEEICVA	ASKACGITPV	YHNMFALMSE	TERIWYPPNH
Consensus	----L-FSG	EYTAE--CI-	AA--CGITP-	CHNLFAL-DE	----WYPPNH
pileup.mfs(Jak1)	IITVDDKTSL	RLHYRMRFYF	TNWHTNDNE	QSVWRHSPKK	QKNGYEKKRV
pileup.msf(Tyk2)	ILEIPRDASL	MLYFRIRFYF	RNWHGMPRE	PAVYRCGPPG	TEASSD..QT
pileup.msf(Jak2)	VFHIDESTRH	DILYRIRFYF	PHWY.....	.....CSGSS	RTYRYGVSRG
Consensus	I--ID--TSL	-L-YRIRFYF	-NWHG-N--E	--V-RCSP--	----Y---R-
pileup.msf(Jak1)	PEATPLLDAS	SLEYLFAQGQ	YDLIKFLAPI	RDPKTEQDGH	DIENECLGMA
pileup.msf(Tyk2)	AQGMQLLDDPA	SFEYLFEQKG	HEFVNDVASL	WELSTEEIHH	HFKNESLGMA
pileup.msf(Jak2)	AEA.PLLDDF	VMSYLFAQMR	HDFVHGWIKV	.....PVTH	ETQEECLGMA
Consensus	AEA-PLLD--	S-EYLFAQG-	HDFV---A--	----TE---H	---NECLGMA
pileup.msf(Jak1)	VLAISHYAMM	KKMQLPELPK	DISYKRYIPE	TLNKSIRQRN	LLTRMRINNV
pileup.msf(Tyk2)	FLHLCHLALR	HGIPLLEEVAK	KTSFKDCIPR	SFRRHIRQHS	ALTRLRLNV
pileup.msf(Jak2)	VLDMMRIAKE	KDQTPAVYN	SVSYKTFLPK	CVRAKIQDYH	ILTRKRIYR
Consensus	VL---H-A--	K---L-EV-K	--SYK--IP-	--R--IRQ--	-LTR-RIRNV

FIG.5A

pileup.ms(Jak1)	FKDFLKEFNN	KTICDSSVST	HDLKVYKYLAT	LETLTkHYGA	EIfETSMlllI
pileup.ms(Jak2)	FRRFLRDFQ.	....PGRlsQ	QMWVWKYLAT	LERLAPRFGT	ERVPVCHLRL
pileup.ms(Jak2)	FRRFIQQF..	...SQCKATA	RNLKLKYLIN	LETLQSAFYT	EQFEV.....
Consensus	FRRFL--F--	-----S-	--LKVKYLAT	LETL---FGT	E-FEV--L--
pileup.ms(Jak1)	SSENELSRCH	SNDS.....	.....GNV	LYEVMVTGNL	GIQWRQXPNV
pileup.ms(Jak2)	LAQAECEPCY	IRDSGVAPTD	PGPESAAAGPP	THEVLVTGTG	GIQWMPVEEE
pileup.ms(Jak2)	.....	.....KE	SARGPSQEEI	FATIIITGNG	GIQWS.....
Consensus	----E---C-	--DS-----	-----G--	--EV-VTNG	GIQWS-----
pileup.ms(Jak1)	VPVEKE....	.....KNKLK	RKKLEYNKHK	KDDERNKLRE	EWNNFSYFPE
pileup.ms(Jak2)	VNKEEGSSGS	SGRNPQASLF	GKKAKAHKAF	GQPADRRPREP	LWAYFCDFRD
pileup.ms(Jak2)	.....	.....	.....RGK	HKESETL TEQ	DVQLYCDFPD
Consensus	V--E-----	-----L-	-KK----K-K	-----E-	-W--FCDFPD
pileup.ms(Jak1)	ITHIVIKE..	.....SVV	SINKQDNKNM	ELKLSSREEA	LSFVSLVDGY
pileup.ms(Jak2)	ITHVWLKE..	.....HCV	SIHRQDNKCL	ELSLPSRAAA	LSFVSLVDGY
pileup.ms(Jak2)	IIDVSIKQAN	QECNESRIV	TVHKQDGKVL	EIELSSLKEA	LSFVSLIDGY
Consensus	ITHVWIKE--	-----V	SIHKQDNK-L	EL-LSSR-EA	LSFVSLVDGY
pileup.ms(Jak1)	FRLTADAHY	LCTDVAPPLI	VHNIQNGCHG	PICTEYAINK	LRQEGSEEGM
pileup.ms(Jak2)	FRLTADSSHY	LCHEVAPPRL	VMSIRDGTHG	PLLEPFVQAK	LR...PEDGL
pileup.ms(Jak2)	YRLTADAHY	LCKEVAPPVAV	LENIHSNCHG	PTSMDFAIK	LKAGNQTGL
Consensus	FRLTADAHY	LC-EVAPP--	V-NI--GCHG	PI---FAI-L	LR--G-E-GL

FIG.5B

pileup.ms f(Jak1)	YVLRW SCTDF	DNILMTVTCG	EKSEVLGGQK	..QNFQIE	VQKFRYSLHG
pileup.ms f(Tyk2)	YLIHWSTSHP	YRLILTVA...	QRSQAPDGMQ	SLRLRKFPPIE	QQDGAFVLEG
pileup.ms f(Jak2)	YVLRCS PKDF	NKYFLTFA.V	ERENVIEYKH	CLITKN....	.ENGEYNLSG
Consensus	YVLRWS--DF	----LTVA--	ERS-V--G--	-L--KNF-IE	-Q-G-Y-L-G
pileup.ms f(Jak1)	SMDHFP SLRD	LMNHLKKQIL	RTDNISFVLK	RCCQPKPREI	SNLLV.....
pileup.ms f(Jak1)	WGRSFPSVRE	LGAALQGCLL	RAGDDCFSLR	RCCLPQGET	SNLIT.....
pileup.ms f(Jak2)	TKRNF SNLKD	LLNCYQMETV	RSDSIIFQFT	KCCPPKPKDK	SNLLVFRTNG
Consensus	--R-FPSLRD	L-N-LQ---L	R-D-I-F-L-	RCC-PKP-E-	SNLLV-----
pileup.ms f(Jak1)	..ATKKAQEW	QPVVSM SQLS	FDRILK KDII	QGEHLGRGTR	THIYSGTLL.
pileup.ms f(Tyk2)	...MRGARAS	PRTLNL SQLS	FHRVDQKEIT	QLSHLGQGTR	TNVYEGRLRV
pileup.ms f(Jak2)	ISDVQISPTL	QRHNNVNQMV	FKIRNEDLI	FNESLGQGTF	TKIFKGVRR
Consensus	-----A---	QR--N-SQLS	FHRI--KDII	Q-EHLGQGTR	T-IY-G-LR-
pileup.ms f(Jak1)	.....D	YKDEEGIAEE	K....KIKVI	LKVLDP SHRD	ISLAFEEAAS
pileup.ms f(Tyk2)	EGSGDPEEGK	MDDEDPLVPG	RDRGQELRVV	LKVLDP SHHD	IALAFYETAS
pileup.ms f(Jak2)	.....	.....VGD	YGQLHKTEVL	LKVLDKAHRN	YSESFEEAAS
Consensus	-----	--DE---V--	-----K--V-	LKVLDP SHRD	ISLAFEEAAS
pileup.ms f(Jak1)	MMRQVSHKHI	VLYYGVCVRD	VENIMVEEFV	EGGPLDLFMH	RKSDAL TTPW
pileup.ms f(Tyk2)	LMSQVSHTHL	AFVHGVCVRG	PENIMVTEYV	EHGPLDVWLR	RERGHVPMAW
pileup.ms f(Jak2)	MMSQLSHKHL	VLNYGVCVCG	EENILVQEFV	KFGSLDTYLK	KNKNSINILW
Consensus	MMSQVSHKHL	V--YGVCVRG	-ENIMV-EFV	E-GPLD--L-	R-----W

FIG.5C

pileup.msf(Jak1)	KFKVAKQLAS	ALSYLEDKDL	VHGNVCTKNL	LLAR.EGIDS	DIGPFIKSLD
pileup.msf(Tykw)	KMVVAQQLAS	ALSYLENKNL	VHGNVCGRNI	LLAR.LGLAE	GTSPFIKSLD
pileup.msf(Jak2)	KLGVAKQLAW	AMHFLEEKSL	IHGNCVAKNI	LLIREEDRRT	GNPPFIKSLD
Consensus	K--VAKQLAS	ALSYLE-L-L	VHGNVC-KNI	LLAR-EG---	G--PFIKSLD
pileup.msf(Jak1)	PGIPVSVLTR	QECIERIPWI	APECVEDSKN	.LSVAADKWS	FGTTLWEICY
pileup.msf(Tyk2)	PGVGLGALSR	EERVERIPWL	APECLPGGAN	SLSTAMDKWG	FGATLLEICF
pileup.msf(Jak2)	PGISITVLPK	DILQERIPWV	PPECIENPKN	.LNLATDKWS	FGTTLWEICS
Consensus	PGI---VL-R	-E--ERIPW-	APEC-E--KN	-LS-A-DKWS	FGTTLWEIC-
pileup.msf(Jak1)	NGEIPLKDKT	LIEKERFYES	RCRPVTPSCK	ELADLMTRCM	NYDPNQRPF
pileup.msf(Tyk2)	DGEAPLQSR	PSEKEHFYQR	APECLPGGAN	QLATLTSQCL	FGATLLEICF
pileup.msf(Jak2)	GGDKPLSALD	SQRKLQFYED	KHQLPAPKWT	ELANLINNCM	FGTTLWEICS
Consensus	-GE-PL----	--EKE-FYE-	-HRLP-PSC-	ELA-L----CM	-YEP-QRP-F
pileup.msf(Jak1)	RAIMRDINKL	.....E	EQN.PDI...	.VSEKQPTTE	VDPTHFEKRF
pileup.msf(Tyk2)	RTILRDLTRL	.....Q	PHNLADV...	.LTVPDSPA	SDPTVFHKRY
pileup.msf(Jak2)	RAVIRDLNSL	FTPDYELLTE	NDMLPNMRIG	ALGFSGAFED	RDPTQFEERH
Consensus	RAI-RDLN-L	-----E	--NLPD----	-L-----	-DPT-FEKR-
pileup.msf(Jak1)	LKKRIRDLGEG	HFGKVELCRY	DPECNTGEQ	VAVSKLPES	GGNHIADLKK
pileup.msf(Tyk2)	LKKIRDLGEG	HFGKVSLEYCY	DPTNDGTGEM	VAVKALKADC	GPQHRSGWKQ
pileup.msf(Jak2)	LKFLQLGKG	NFGSVMCRY	DPLQDNTGEV	VAVKKLQ.HS	TEEHLRDFER
Consensus	LK-IRDLGEG	HFGKVELCRY	DP--DNTGE-	VAVK-LK--S	G--H--D-K-

FIG.5D

pileup.ms(Jak1)	EIEILRNLYH	ENIVKYKGIC	MEDGGNGIKL	IMEFLPSGSL	KEYLPKNKKNK
pileup.ms(Jak2)	EIDILRTLHY	EHIKYKGCC	EDQGEKSLQL	VMEYVPLGSL	RDYLP..RHS
pileup.ms(Jak2)	EIEILKSLQH	DNVYKGVCC	YSAGRRNLRL	IMEYLPYGSL	RDYLQKHKE
Consensus	EIEILR-LYH	ENIVKYKG-C	---G---L-L	IMEYLP-GSL	RDYLPK-K--
pileup.ms(Jak1)	INLKQQLKYA	IQICKGMDYL	GSRQYVHRDL	AARNLVESE	HQVKIGDFGL
pileup.ms(Jak2)	IGLAQLLLFA	QQICECMAYL	HAQHYIHRDL	AARNVLLDND	RLVKIGDFGL
pileup.ms(Jak2)	IDHKLLQYT	SOICKGMEYL	GTKRYIHRDL	ATRNILVENE	NRVKIGDFGL
Consensus	I-LKQLL-YA	-QICKGM-YL	G---YIHRDL	AARNLVENE	--VKIGDFGL
pileup.ms(Jak1)	TKAIETDKEY	YTVKDDRDSP	VFWYAPECLI	QCKFYIASDV	WSFGVTLHEL
pileup.ms(Jak2)	AKAVPEGHEY	YRVREDGDS	VFWYAPECLK	EYKFYASDV	WSFGVTLYEL
pileup.ms(Jak2)	TKVLPQDKEY	YKVKEPGES	IFWYAPESLT	ESKFSVASDV	WSFGVVLVEL
Consensus	TAK-P-DKEY	Y-VKEDGDS	VFWYAPECL-	ESKFSVASDV	WSFGVVLVEL
pileup.ms(Jak1)	LYCDSDFS	MALFLKMTGP	T.HGQMTVTR	LVNTLKEGKR	LPCPPNCPDE
pileup.ms(Jak2)	LTHCDSSQSP	PTKFLELIGI	A.QGQMTVLR	LTELLERGER	LPRPKCPCE
pileup.ms(Jak2)	FTYIEKSKSP	PVEFMRMIGN	DKQGMIVFH	LIELLSKNGR	LPRPEGCPDE
Consensus	LYCDSS-SP	P--FL-MIG-	--QGQMTV-R	L-ELLK-G-R	LPRP--CPDE
pileup.ms(Jak1)	VYQLMRKCWE	FQPSNRTTFQ	NLIEGFEALL	K.....	.....
pileup.ms(Jak2)	VYHLMKNCWE	TEASFRPTFE	NLIPILKTVH	EKYQGQAPSV	FSVC*
pileup.ms(Jak2)	IYVIMTECWN	NNVSQRPSFR	DLSGWIKSG	TVI.....	.....
Consensus	VY-LM--CWE	---S-RPTF-	NLI-G-----	-----	-----

FIG.5E

JAK3	1	11	21	31	41	51	61	71	81	91
JAK2	M.	APPSEETPLIPQ	SCSLSSSEACALHVL	PPRGPQQRLSF	SFGDYLAE	DLCVRAAKACG	ILPVVHSLF	ALATEDF	SCWFP	PSH
JAK1	MQMACL	TMTEATSTSPV	HQNGDIPGSANS	VKQIEPV	LOVLYHSL	GQAGEYLK	FPSEGYVAEE	ICVAASKACG	ITPVYHNM	FALMSETERIWYPPNH
TYK2	MQYLN	KEDCNAMAFCA	KMRSFKKTEV	KQVPEP	.GVEVTFYLLDR	.EP	.LRLGSGEY	TAEEELCIRAAQEC	SIPLCHNLF	FALYDESTKLWYAPNR
CON	MPLRHW	.....	GMARGSKPV	GGAQPMAMGGL	KVLLHWAG	PGGEP	.WTFSESSL	TAEEVCIHIAHKVG	ITPPCFNL	FALFDAQAQVWLPPNH
	M	.....	G	EP	L.F	.G.Y	.AEE	C.AA	.CGI	P.HNLFAL
JAK3	101	111	121	131	141	151	161	171	181	191
JAK2	IFCIEDVD	TQVLVYRLRF	YFPDWF	.....	GLETCHRF	GLRKDLTS	.A	LDLHVLEHLF	AQHRSDLV	SGRLPV
JAK1	VFHIDEST	RHDILYRIRF	YFPHWY	.....	CSCSSRTY	RYGVSRC	AELPLDDF	VMSYLF	AQWRHDF	VHGWI
TYK2	IIITVDDK	TSRLHYRMRF	YFTNWHG	TNDNEQ	SVWRHSPK	KQNGYE	KKRVPEAT	PLLDASS	LEYLFA	CGQYDL
CON	ILEIPRDA	SLMLYFRIRF	YFRNWHGM	PREP	AVYRCPPG	TEASSDQT	.A	QGMQLDP	ASFEYLF	EQGKHEFV
	I	.....	L	YR	RFYF	.W	.....	LLD	.....	EYLFAQ
JAK3	201	211	221	231	241	251	261	271	281	291
JAK2	VLDLAQ	AREQAQR	PGCELLKTV	SYKACLP	PSLRDVI	QQNFVTRRR	IR.....	RTWLALP	.....	CGRLPG
JAK1	VLDMMRI	AKEKQOTPL	AVNSYK	TFLPK	CVRAKIQ	DYHIL	TRKIRY	RFRF	IQQFSQ	.....
TYK2	VLAISHY	AMMKQ	PEL	PKDIS	YKRYI	PETL	INKSIR	QNLTRM	RINNV	KDFL
CON	FLHLCH	LALRHG	I	PLEE	VAKTSF	KDCIP	RSFR	RH	IOH	SAL
	VL	.....	A	.....	E	K	SYK	.....	P	.....
JAK3	301	311	321	331	341	351	361	371	381	391
JAK2	.....	GL	.....	PGAE	EPL	.....	LRVAG	NGIPW	.....	SS
JAK1	.....	KES	AR	PSGEE	IFAT	.....	IIITG	NGIQW	.....	SRGK
TYK2	LLTISSE	NELSR	CHSND	.....	SGNVLYE	VMVTG	NLGI	QWRQ	KPNV	VEKEKN
CON	LLAQAE	GEP	CYIR	DSG	VAP	TD	PG	ESA	GP	PTHE
JAK3	401	411	421	431	441	451	461	471	481	491
JAK2	EIVDVS	INQAP	RVGPAGE	HRLVT	ITRMD	G	CHILEA	EPGL	PEAL	SFVAL
JAK1	DIIDVS	IKOANQ	.ECSN	ESRIV	TVHK	QDKVLE	IELSSL	KEAL	SFVSL	IDGYR
TYK2	EITHIV	IK	.....	SVVS	INKD	KNMEL	KLSS	REEAL	SFVSL	VDGYR
CON	DITHVL	KE	.....	HCVS	IHRQ	DNK	CLEL	SLPS	RAAL	SFVSL
	I	V	JK	.....	V	.....	QD	K	LE	L

FIG. 6A



501	511	521	531	541	551	561	571	581	591
JAK3	GTYLRRSPQDYDSFLLTA	CVQTPGLPDYKGLIRQD	.....	PSGAFSLVGLSQPHRSLRELLAACWN	SGLRVQGAALYL	TSCCAPRPEKSNL	IWR		
JAK2	GLYLRCSPKDFNKYFLTF	AVERENVIEYKHLITKN	.....	ENGEYNLSGTRNF	SNLKDLLN	CYQMETVRSDSIT	TFQFTKCCPPKPKDKSNLLVFR		
JAK1	GMVLRWSCDFDNILMTVTCFKESE	VLGGQK	QFKNFQIEVQKGRYSLHGSMDHFP	PSLRDLNMH	LKKQILRTDNISFVL	KRCCQPKPRE	ISNLLVA		
TYK2	GLYLHWSTSHPYRLILTVA	..QRSQAPDGMQSLRLRKFPIEQDDGAFV	LEGWGRSFP	PSVRELGA	..LQGLLRAGDDCF	SLRRCCLPQGETSNL	IIM		
CON	G.Y.LR.S.D.....LT	.....L	.....G	..L.G	.....F	SLR.L	.....LR.D	..F.L	..CC.P.P.E.SNL.V
601	611	621	631	641	651	661	671	681	691
JAK3	RGCNPAPAGCSPSCCAL	TQLSFHTIPTDSLEWHENLHGCSFTKIFGRSRRE	.....	VVD	..GETHSEVLLKVMDSRHRNOMESF				
JAK2	TNGISDVQISPTLQRHNNVQWVFHK	IRNEDL	IFNESLGGQFTKIFKGVRR	.....	VGDYQQLHKTEVLLKVL	DKAHRNYESF			
JAK1	.....TKKAQEWQPVYMSQLS	FDRIILKKOI	IQGEHLGRGTRTHIYSGTLLDYKDEEGIAEKKI	.....	KVILKVLDP	SHRDISLAF			
TYK2	.....RCARASPTLNLSQ	SFHRVDQKEITQLSHLGGQTRTNVYEGRLRV	..EGSGDPEEGKMDDEDPLV	PGDRGQELRVVL	KVLDPSHHDIALAF				
CON	.....QLSFH.I	.....E.LG	GT.T.I	..G.R	.....V	.....V.LKVL	..HR	.....F	
701	711	721	731	741	751	761	771	781	791
JAK3	LEAASLMSQVSYPHL	VLLHGVCMAGD	SIMVQEFVYLGAIDMYLKRGRHL	VSASWKLQVTKQALAYALNYLEDKGL	PHGNVSARKVLLAREGG	..DGNPPF			
JAK2	FEAASMSQLSHKHL	VLNYGVCVCGEENIL	VQEFVKFGLDYLKKNKNSINIL	WKLGVAQKQALAWAMHF	LEEKSLIHGNVCAKNILL	IREDRRTGNPPF			
JAK1	FEAASMRQVSHKHI	VYLYGVCVRDVENIMVEEF	VEGGPLDMRKSDAL	TPWKFVKVAKQALASAL	SYLEDKDLVHGNVCTKNLLAREGID	SDIGPF			
TYK2	YETASLMSQVSHTHLAF	VHGVCVRGVPENSMWTEYVEHGPLDWL	RRERGHVPMWKMVVAQQLASALSYLENKNL	VHGNVCGRNILLARGLA	EGTSPF				
CON	EAAS.MSQVSH.HLV	..GVCV	G.ENIMV.EFV	..G.LD	.....WK	..VA	QLA.AL	..YLE	..K.L.HGNVC
									..N.LLAREG
801	811	821	831	841	851	861	871	881	891
JAK3	IKLSDPGVSPVLSLEML	TDRIPWVAPECL	QEAQTLCLEADKNGFGATTWEV	FQRPAGHI	TSLEPAKKLFYEDQQL	PALKWTEL	AGLITQCMAYDPG		
JAK2	IKLSDPGISITVL	PKDILQERIPWVPECI	ENPKNLNLA	TDKWSFGTTLWE	ICSGGDKPLSALDSQRKLQF	YEDKHQLPAPKWTEL	ANLINNCMDYEPD		
JAK1	IKLSDPGIPVSVL	TRQECIERIPWIAPECV	EDSKNLSVAADKWSFGTTLWE	ICYNGEIP	LPDKTLIEKERFYESRCRPVTP	SCKELADL	TRCMNYDPN		
TYK1	IKLSDPGIGL	GALSREERVERIPWL	APECLPGCANSL	STAMDKNGFGATLLE	ICFDGEAPLQSRSPSEKEHF	YQRQHLRPEP	SCPQLATLTSQCLTYEPT		
CON	IKLSDPGI...VL	.....ERIPW	APEC	.....L	..A.DKW	FG.TLWEIC	..G.PL	.....K	..FYE
									.....LP.P
									..ELA.L
									..CM.Y.P

FIG.6B

901 911 921 931 941 951 961 971 981 991  
 JAK3 RRPFRATILRDNLGITSYELLSDPTGIPSPRDELCAAGLAQYACQDPAIFEEHRLKYISLLGKNGFSGVELCRYDPLGDNLTGTLVAVKQLQ.HSVPD  
 JAK2 FRPAFRVIRDLNSLTPDYELLTENDM.LPNMRIGALGF.SCAFEDRDPTQFEERHLKFLQQLGKNGFSGVMCRYDPLQDNTGEVAVKKLQ.HSTEE  
 JAK1 QRPFFRAIMRDINKLEEQN.PDI VSEKQP.....TTEVDPTHFEKRF.LKRI.RDLGEGHFGKVELCRYDPEGDNTEGEQVAVKSLKPESGGN  
 TYK2 QRPSEFTILRDLTRVQPHNLADVLTVNRDSP.....A.VGPTTFHKRYLKKIRDLGEGHFGKVSLEYDPTNDGTCEMWAVKALKADCGPQ  
 CON .RP.FRAI.RDLN.L.....P.....PT.FE.R.LK.I..LG.G.FG.VELCRYDP..DNTGE.VAVK.L.....S....

1001 1011 1021 1031 1041 1051 1061 1071 1081 1091  
 JAK3 QQRDFQREIQILKALHSDFIVKYRGVSYGPGRQSLRLVMEYLPSCGLRDLLOQRHC.LHTDRLLFAWQICKGMEYLGAARRCVHRDLAARNILVESEAHV  
 JAK2 HLRDFEREIEILKSLQHDNIVKYKGVCSAGRRNRLIMEYLPYCSLRDYLQKHKERIDHKLLQYTSQICKGMEYLGTKRYIHRDLATRNILVENENRV  
 JAK1 HIADLKEIEILRNLYHENIVKYKGIOMEDEGNGIKLIMEFLPSGSLKEYLPKKNKINLKQQLKYAIOICKGMDYLGSRQYVHRDLAARNVLVESEHQV  
 TYK2 HRSGWKQEIIDLRTL YEHI IKYKGCCEDEQCEKSLQLVMEYPLGSLRDYLPRHS..IGLAQLLLFAQQICEGMAYLHAHDYIHRDLAARNVLLDNDRLV  
 CON H..D....EI..IL..L.H..IVKYKG.C...G...L.L.MEYLP.GSLRDYL..H...I....LL..A.QICKGM.YLG...Y.HRDLAARN.LVE.E..V

1101 1111 1121 1131 1141 1151 1161 1171 1181 1191  
 JAK3 KIADFGLAKLLPLGKDYVVRPQGQSPFIWYAPESLSDNIFSRQSDVWSFGVLYELFTYCDKSCSPSAEFLRMGPEREGPPLC.RLLELLAEGRRLLPP  
 JAK2 KIGDFGLTKVLPQDKEYKVKKEPCESPFIWYAPESL TESKFSVADVWSFGVLYELFTYIEKSKSPPEFMRMIGNDKQGMIVFHLIELLSNGRLPR  
 JAK1 KIGDFGLTKAETDKEYYTVKDDRDSPVWYAPECLIQCKFYIASDVWSFGVTLHELLTYCDSDFSFMALFLKMIGPT.HGQMTVTRLVNTLKEGKRLPC  
 TYK2 KIGDFGLAKAVPEGHEYYRVREDGDSPIWYAPECLKEYFYASDVWSFGVTLYELLTHCDSSQSPPTKFLLELIGIA.QGQMTVLRLTTELLERGERLPR  
 CON KIGDFGL.K..P..KEYY.V.E.G.SP.FWYAPE.L...KF..ASDVWSFGV.LYEL.TYCD.S.SP...FL.MIG.....GQM.V.V.RL.ELL..G.RLP.

1201 1211 1221 1231 1241  
 JAK3 PPTCPTVQELMQLCWAPEPHDRPAFATLSPQLDPLW.RG.....RPG\*  
 JAK2 PEGCPDEIYVIMTECWNVNSQRPFRDL.SFG.....WIKS.....GTV\*  
 JAK1 PPNCPEVYQLMRKCWEFQPSNRITTFQNLIEGFEALLK\*  
 TYK2 PDKCPCEVYHLMKNCWETEASFRPTFENLIPILKTVHEKYQGQAPSVFSVC\*  
 CON P..CP.EVY.LM..CW.....S.RP.F.L.....

FIG. 6C

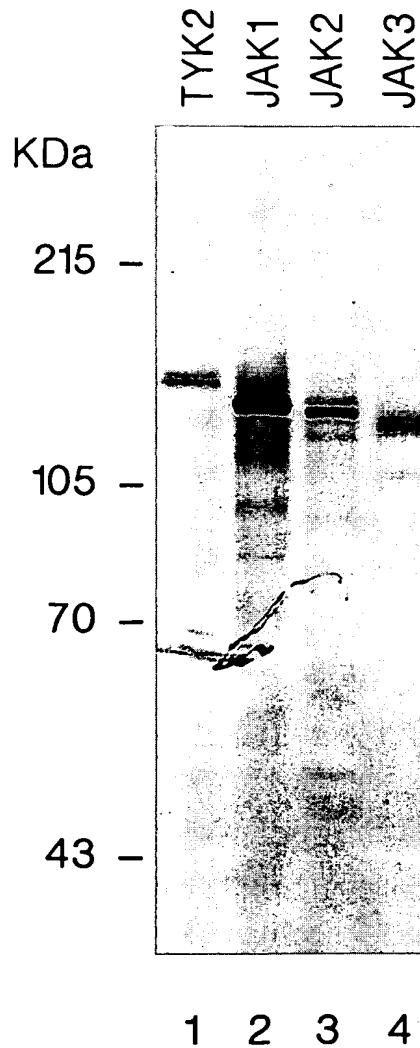


FIG.7A

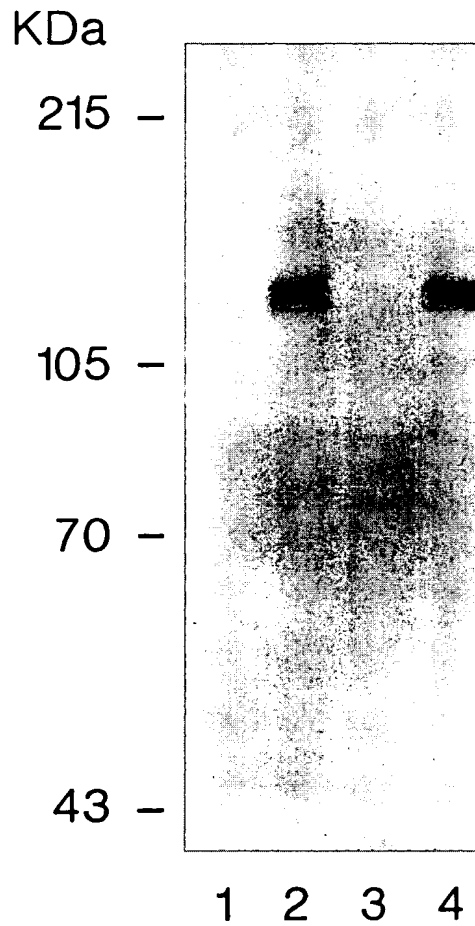


FIG.7B

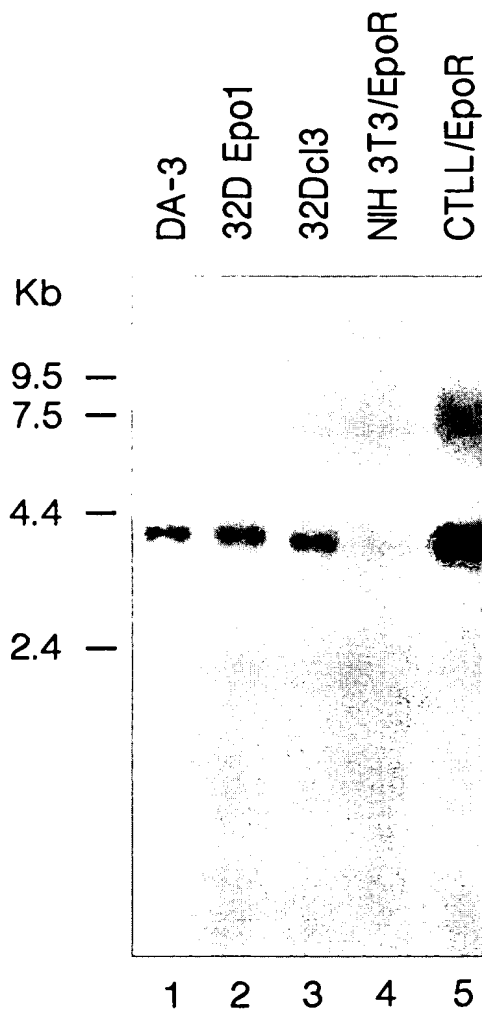


FIG.8

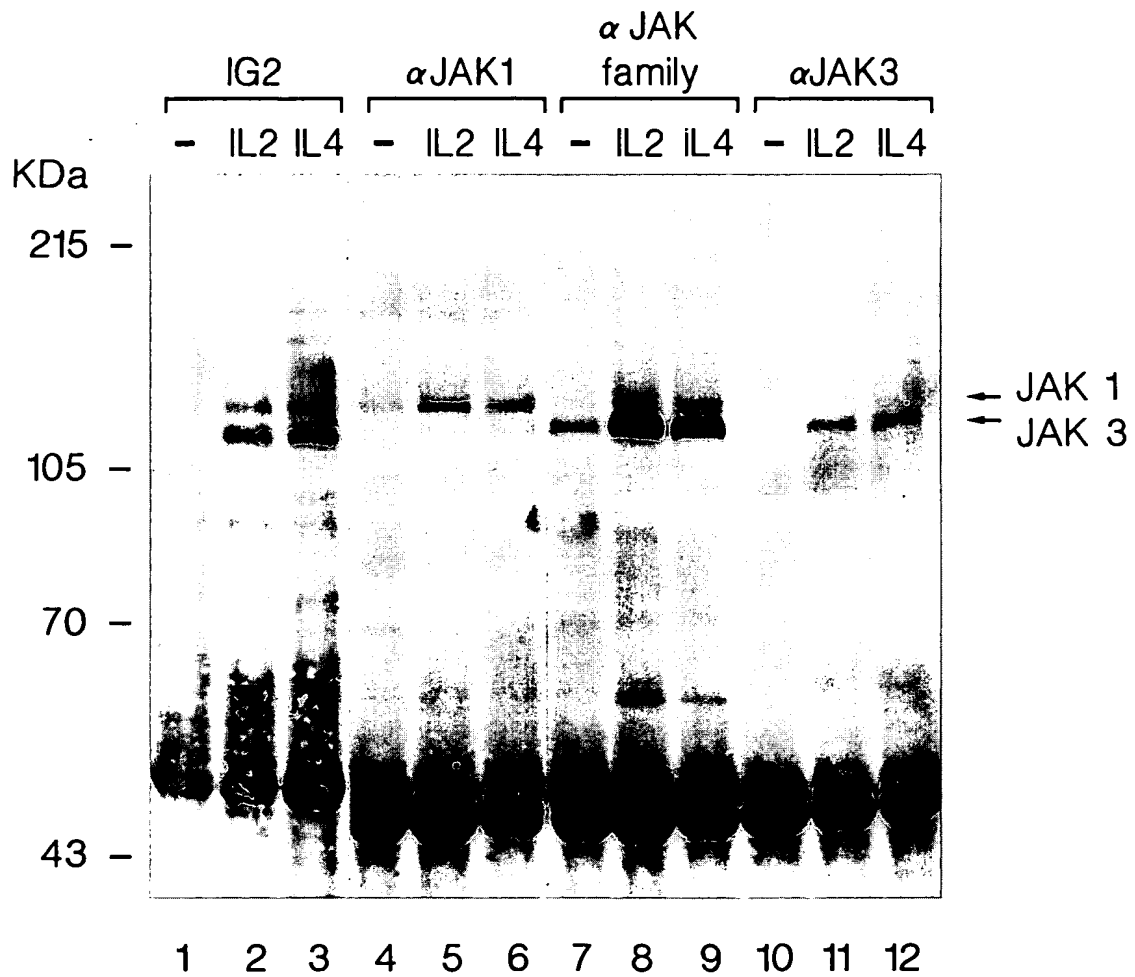


FIG.9A

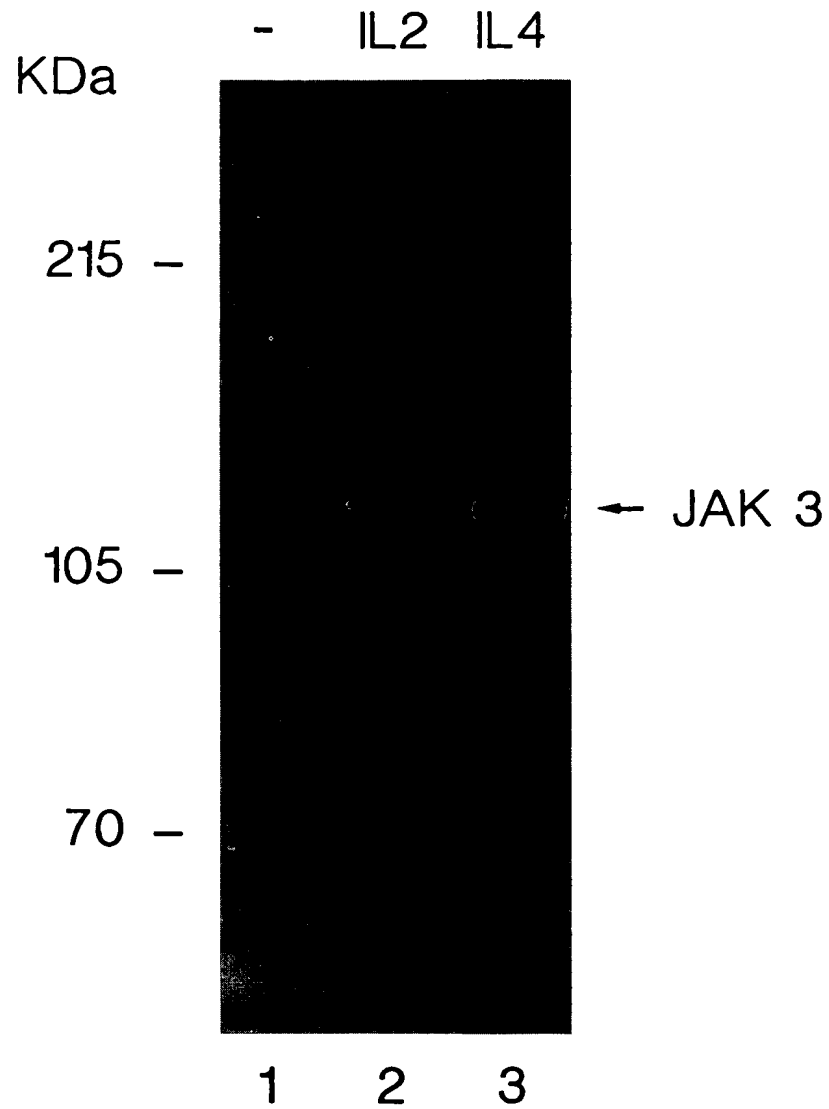


FIG.9B

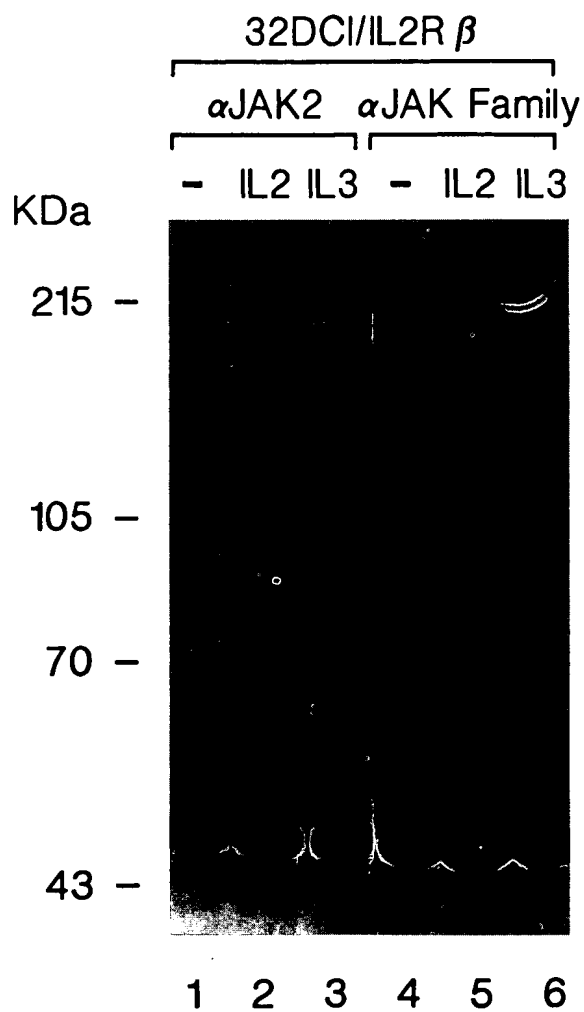


FIG.9C



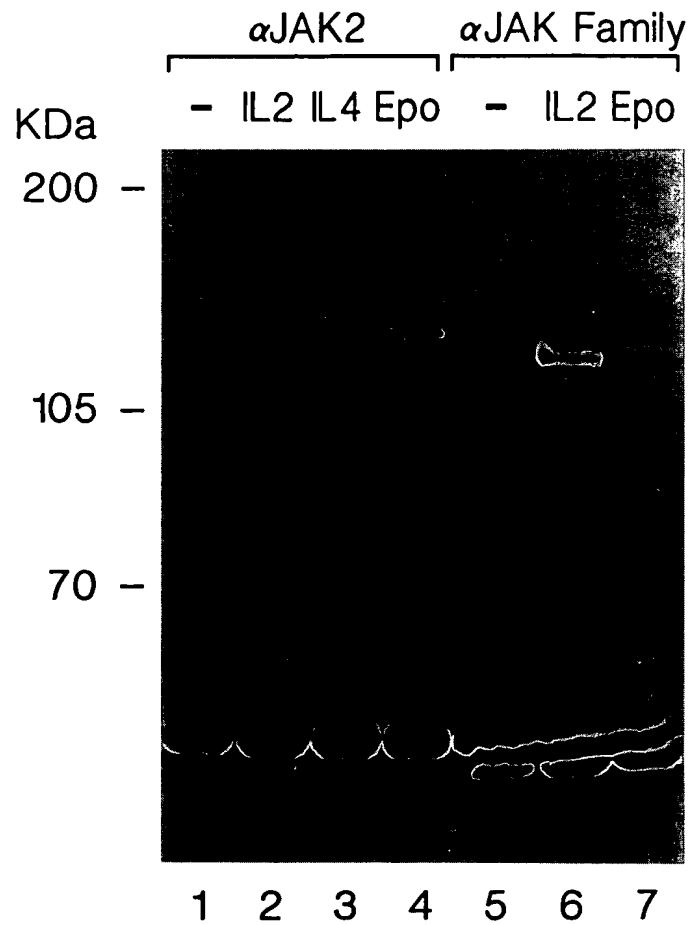


FIG.9D

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